OIPE

INPUT SET: S34917.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages

ENTERED

```
 1                              SEQUENCE LISTING
 2
 3   (1)      General Information
 4
 5            (i) APPLICANT: Au-Young, Janice
 6                          Lal, Preeti
 7                          Bandman, Olga
 8
 9            (ii) TITLE OF THE INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
10
11            (iii) NUMBER OF SEQUENCES: 7
12
13            (iv) CORRESPONDENCE ADDRESS:
14               (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15               (B) STREET: 3174 Porter Drive
16               (C) CITY: Palo Alto
17               (D) STATE: CA
18               (E) COUNTRY: USA
19               (F) ZIP: 94304
20
21            (v) COMPUTER READABLE FORM:
22               (A) MEDIUM TYPE: Diskette
23               (B) COMPUTER: IBM Compatible
24               (C) OPERATING SYSTEM: DOS
25               (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27            (vi) CURRENT APPLICATION DATA:
28               (A) APPLICATION NUMBER: To Be Assigned
29               (B) FILING DATE: Herewith
30
31            (vii) PRIOR APPLICATION DATA:
32               (A) APPLICATION NUMBER: 08/868,288
33               (B) FILING DATE: June 3, 1997
34
35               (A) APPLICATION NUMBER: 09/235,373
36               (B) FILING DATE: January 20, 1999
37
38               (A) APPLICATION NUMBER: 09/388,993
39               (B) FILING DATE: September 2, 1999
40
41            (viii) ATTORNEY/AGENT INFORMATION:
42               (A) NAME: Streeter, David G.
43               (B) REGISTRATION NUMBER: 43,168
44               (C) REFERENCE/DOCKET NUMBER: PF-0309-3 DIV
45
46            (ix) TELECOMMUNICATION INFORMATION:
```

INPUT SET: S34917.raw

```
47              (A) TELEPHONE: 415-855-0555
48              (B) TELEFAX: 415-849-8886
49
50
51          (2) INFORMATION FOR SEQ ID NO:1:
52
53          (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 358 amino acids
55              (B) TYPE: amino acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59          (vii) IMMEDIATE SOURCE:
60              (A) LIBRARY: SYNORAB01
61              (B) CLONE: 136466
62
63          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65      Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
66       1               5                  10                  15
67      Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
68                   20                  25                  30
69      Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
70               35                  40                  45
71      Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
72           50                  55                  60
73      Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
74      65                  70                  75                  80
75      Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
76                   85                  90                  95
77      Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
78                   100                 105                 110
79      Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
80               115                 120                 125
81      Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
82           130                 135                 140
83      Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
84      145                 150                 155                 160
85      Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
86                   165                 170                 175
87      Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
88                   180                 185                 190
89      Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
90                   195                 200                 205
91      Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
92           210                 215                 220
93      Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
94      225                 230                 235                 240
95
96      Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
97                   245                 250                 255
98      Asp Leu Tyr Thr Asn Val Thr Val Ser Leu Val Glu Ser Leu Val Gly
99                   260                 265                 270
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INPUT SET: S34917.raw

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100      Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
101          275                 280                 285
102      Arg Asp Lys Ile Thr Arg Pro Gly Ala Xaa Xaa Trp Lys Lys Gly Glu
103          290                 295                 300
104      Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
105      305                 310                 315                 320
106      Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
107                  325                 330                 335
108      Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
109              340                 345                 350
110      Asn Gly Leu Gln Gly Tyr
111          355
112
113              (2) INFORMATION FOR SEQ ID NO:2:
114
115          (i) SEQUENCE CHARACTERISTICS:
116              (A) LENGTH: 1376 base pairs
117              (B) TYPE: nucleic acid
118              (C) STRANDEDNESS: single
119              (D) TOPOLOGY: linear
120
121          (vii) IMMEDIATE SOURCE:
122              (A) LIBRARY: SYN0RAB01
123              (B) CLONE: 136466
124
125          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
126
127      TCTCACCGGG ACTCGGGACT CCCGGGAAGT GGACCGGCAG AAGAGGGGGC TAGCTAGCTG      60
128      TCTCTGCGGA CCAGGGAGAC CCCCGCGCCC CCCCGGTGTG AGGCGGCCTC ACAGGGCCGG     120
129      GTGGGCTGGC GAGCCGACGC GGCGGCGGAG GAGGCTGTGA GGAGTGTGTG GAACAGGACC     180
130      CGGGACAGAG GAACCATGGC TCCGCAGAAC CTGAGCACCT TTTGCCTGTT GCTGCTATAC     240
131      CTCATCGGGG CGGTGATTGC CGGACGAGAT TTCTATAAGA TCTTGGGGGT GCCTCGAAGT     300
132      GCCTCTATAA AGGATATTAA AAAGGCCTAT AGGAAACTAG CCCTGCAGCT TCATCCCGAC     360
133      CGGAACCCTG ATGATCCACA AGCCCAGGAG AAATTCCAGG ATCTGGGTGC TGCTTATGAG     420
134      GTTCTGTCAG ATAGTGAGAA ACGGAAACAG TACGATACTT ATGGTGAAGA AGGATTAAAA     480
135      GATGGTCATC AGAGCTCCCA TGGAGACATT TTTTCACACT TCTTTGGGGA TTTTGGTTTC     540
136      ATGTTTGGAG GAACCCCTCG TCAGCAAGAC AGAAATATTC CAAGAGGAAG TGATATTATT     600
137      GTAGATCTAG AAGTCACTTT GGAAGAAGTA TATGCAGGAA ATTTTGTGGA AGTAGTTAGA     660
138      AACAAACCTG TGGCAAGGCA GGCTCCTGGC AAACGGAAGT GCAATTGTCG GCAAGAGATG     720
139      CGGACCACCC AGCTGGGCCC TGGGCGCTTC CAAATGACCC AGGAGGTGGT CTGCGACGAA     780
140      TGCCCTAATG TCAAACTAGT GAATGAAGAA CGAACGCTGG AAGTAGAAAT AGAGCCTGGG     840
141      GTGAGAGACG GCATGGAGTA CCCCTTTATT GGAGAAGGTG AGCCTCACGT GGATGGGGAG     900
142      CCTGGAGATT TACGGTTCCG AATCAAAGTT GTCAAGCACC CAATATTTGA AAGGAGAGGA     960
143      GATGATTTGT ACACAAATGT GACAGTCTCA TTAGTTGAGT CACTGGTTGG CTTTGAGATG    1020
144      GATATTACTC ACTTGGATGG TCACAAGGTA CATATTTCCC GGGATAAGAT CACCAGGCCA    1080
145      GGAGCGAANT ANTGGAAGAA AGGGGAAGGG CTCCCCAACT TTGACAACAA CAATATCAAG    1140
146      GGCTCTTTGA TAATCACTTT TGATGTGGAT TTTCCAAAAG AACAGTTAAC AGAGGAAGCG    1200
147      AGAGAAGGTA TCAAACAGCT ACTGAAACAA GGGTCAGTGC AGAAGGTATA CAATGGACTG    1260
148      CAAGGATATT GAGAGTGAAT AAAAATTGGAC TTTGTTTAAA ATAAGTGAAT AAGCGATATT    1320
149      TATTATCTGC AAGGTTTTTT TGTGTGTGTT TTTGTTTTTA TTTTCAATAT GCAAGT        1376
150
151              (2) INFORMATION FOR SEQ ID NO:3:
152
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INPUT SET: S34917.raw

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153        (i) SEQUENCE CHARACTERISTICS:
154           (A) LENGTH: 330 amino acids
155           (B) TYPE: amino acid
156           (C) STRANDEDNESS: single
157           (D) TOPOLOGY: linear
158
159        (vii) IMMEDIATE SOURCE:
160           (A) LIBRARY: HNT2RAT01
161           (B) CLONE: 260873
162
163        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
164
165     Met Val Asp Tyr Tyr Glu Val Leu Gly Val Gln Arg His Ala Ser Pro
166      1               5                  10                  15
167     Glu Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys Trp His Pro
168              20                  25                  30
169     Asp Lys Asn Pro Glu Asn Lys Glu Glu Ala Glu Arg Lys Phe Lys Gln
170              35                  40                  45
171     Val Ala Glu Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Asp Ile
172          50                  55                  60
173     Tyr Asp Lys Tyr Gly Lys Glu Gly Leu Asn Gly Gly Gly Gly Gly Gly
174      65                  70                  75                  80
175     Ser His Phe Asp Ser Pro Phe Glu Phe Gly Phe Thr Phe Arg Asn Pro
176                  85                  90                  95
177     Asp Asp Val Phe Arg Glu Phe Phe Gly Gly Arg Asp Pro Phe Ser Phe
178              100                 105                 110
179     Asp Phe Phe Glu Asp Pro Phe Glu Asp Phe Phe Gly Asn Arg Arg Gly
180              115                 120                 125
181     Pro Arg Gly Ser Arg Ser Arg Gly Thr Gly Ser Phe Phe Ser Ala Phe
182          130                 135                 140
183     Ser Gly Phe Pro Ser Phe Gly Ser Gly Phe Ser Ser Phe Asp Thr Gly
184      145                 150                 155                 160
185     Phe Thr Ser Phe Gly Ser Leu Gly His Gly Gly Leu Thr Ser Phe Ser
186                  165                 170                 175
187     Ser Thr Ser Phe Gly Gly Ser Gly Met Gly Asn Phe Lys Ser Ile Ser
188                  180                 185                 190
189     Thr Ser Thr Lys Met Val Asn Gly Arg Lys Ile Thr Thr Lys Arg Ile
190              195                 200                 205
191     Val Glu Asn Gly Gln Glu Arg Val Glu Val Glu Glu Asp Gly Gln Leu
192          210                 215                 220
193     Lys Ser Leu Thr Ile Asn Gly Val Ala Asp Asp Asp Ala Leu Xaa Glu
194      225                 230                 235                 240
195     Glu Arg Met Arg Arg Gly Gln Asn Val Leu Pro Ala Gln Pro Ala Gly
196                  245                 250                 255
197     Leu Arg Pro Pro Lys Pro Pro Arg Pro Ala Ser Leu Leu Arg His Xaa
198              260                 265                 270
199     Pro His Cys Leu Ser Lys Glu Glu Gly Glu Gln Asp Arg Pro Trp Ala
200              275                 280                 285
201     Pro Xaa Xaa Trp Xaa Pro Leu Ala Ser Xaa Ala Gly Xaa Xaa Glu Gly
202          290                 295                 300
203     Xaa Lys Arg Met Xaa Ala Glu Ala Glu Arg Gly Val Glu Glu Glu Glu
204      305                 310                 315                 320
205     Val Asp Gln Arg Gln Ser Leu Asp Arg Thr
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/501,714

INPUT SET: S34917.raw

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206                 325               330
207
208         (2) INFORMATION FOR SEQ ID NO:4:
209
210     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 1330 base pairs
212         (B) TYPE: nucleic acid
213         (C) STRANDEDNESS: single
214         (D) TOPOLOGY: linear
215
216     (vii) IMMEDIATE SOURCE:
217         (A) LIBRARY: HNT2RAT01
218         (B) CLONE: 260873
219
220
221     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
222
223
224  CGNAGGAGAG NAAAGGAAAG NCGCCGCAGG AGCCGCCGCN ACCACCAGCG NCACANTCCT        60
225  GGNGCTNTGA GGAGATTCGG GCCGTCACCC TGCCTCCCCT GCTTCCCGCC ACCGGCCGCT       120
226  TCTTTCCTCG GACCCATTCC AACAATCTCG TAAAACATGG TGGATTACTA TGAAGTTCTA       180
227  GGCGTGCAGA GACATGCCTC ACCCGAGGAT ATTAAAAAGG CATATCGGAA ACTGGCACTG       240
228  AAGTGGCATC CAGATAAAAA TCCTGAGAAT AAAGAAGAAG CAGAGAGAAA ATTCAAGCAA       300
229  GTAGCGGAGG CATATGAAGT GCTGTCGGAT GCTAAGAAAC GGGACATCTA TGACAAATAT       360
230  GGCAAAGAAG GATTAAATGG TGGNGGNGGN GGTGGAAGTC ATTTTGACAG TCCATTTGAA       420
231  TTTGGCTTCA CATTCCGTAA CCCAGATGAT GTCTTCAGGG AATTTTTTGG TGGAAGGGAC       480
232  CCATTTTCAT TTGACTTCTT TGAAGACCCT TTTGAGGACT TCTTTGGGAA TCGAAGGGGT       540
233  CCCCGAGGAA GCAGAAGCCG AGGGACGGGG TCGTTTTTCT CTGCGTTCAG TGGATTTCCG       600
234  TCTTTTGGAA GTGGATTTTC TTCTTTTGAT ACAGGATTTA CTTCATTTGG GTCACTAGGT       660
235  CACGGGGGCC TCACTTCATT CTCTTCCACG TCATTTGGTG GTAGTGGCAT GGGCAACTTC       720
236  AAATCGATAT CAACTTCAAC TAAAATGGTT AATGGCAGAA AAATCACTAC AAAGAGAATT       780
237  GTCGAGAACG GTCAAGAAAG AGTAGAAGTT GAAGAAGATG GCCAGTTAAA GTCCTTAACA       840
238  ATAAATGGTG TKGCCGACGA CGATGCCCTC GSTGAGGAGC GCATGCGGAG AGGCCAGAAC       900
239  GTCCTGCCAG CCCAGCCTGC CGGCCTCCGA CCGCCGAAGC CGCCCCGGCC TGCCTCGTTG       960
240  CTGAGACACG NGCCTCATTG TCTCTCTAAG GAGGAGGGCG AGCAGGACCG ACCTTGGGCA      1020
241  CCCGNGNCCT GGNNCCCCCT CGCTTCCNCA GCAGGNTTNN AAGAAGGTNG CAAGAGGATG      1080
242  NAAGCAGAAG CAGAGAGAGG AGTCGAAGAA GAAGAAGTCG ACCAAAGGCA ATCACTAGAC      1140
243  CGGACTTGAG GCACGCGGTG CACCCCCAGA CGCTGGCGCT CCACCGTGCT CGGCATGCGG      1200
244  TCGTGCACAC GCGCTAGGTA GCAGCGTCGG TCAGGACTGT CTCGAGGCCA CACTCGCTCG      1260
245  GCAGGATTAT GCGATCACGG ATCAGTCAGA GCAGGGTCAG GAGACGGGGC TGACGGCACG      1320
246  GGTGGCGGGG                                                            1330
247
248         (2) INFORMATION FOR SEQ ID NO:5:
249
250     (i) SEQUENCE CHARACTERISTICS:
251         (A) LENGTH: 397 amino acids
252         (B) TYPE: amino acid
253         (C) STRANDEDNESS: single
254         (D) TOPOLOGY: linear
255
256     (vii) IMMEDIATE SOURCE:
257         (A) LIBRARY: GenBank
258         (B) CLONE: 306714
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/501,714*

INPUT SET: S34917.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned